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Oskar R. Zaborsky, Ph.D.
Board on Biology
National Research Council
National Academy of Sciences
2101 Constitution Avenue, N.W.
Washington, D.C. 20418

Dear Oskar:

As I see it, we have three suggestions for recommendations coming out of Chapter 3 (or at least 3 main recommendations).

1) The counting method (1/N method): This applies to the frequency of the complete multi-locus genotype, with N=number of perons in the database, and might be a value of no more than 1/1000. This approach permits experts also to render an opinion that the probability is much lower and to give, in association with that, an estimate based on use of the multiplication rule.

This is the recommendation that is now recorded in Chapter 3 of the most recent draft.

2) Use the multiplication rule and until appropriate population data can be collected use 10% as the ceiling frequency (minimal frequency). This is the suggestion of Paul Ferrara. This would give a minimum likelihood of a chance match, when 4 loci (8 alleles) are used, of 1: 6,250,000.

3) Apply the multiplication rule to data from each of the three major ethnic groups (Caucasian, Afro-American, Mexican-American) and give a range. This is the approach suggested by Caskey who seems dubious about the necessity to do population studies of the type proposed.

It is important to emphasize that these considerations apply only to the VNTR-type loci. VNTR-based tests now used, which test for variation at several, (usually 4) separate loci on different chromosomes.

My own feeling, after much cogitation, is that the 1/N method is excessively conservative and may be confusing in the court setting, and that approach 2 is preferable providing it is well agreed that population studies will be done.

It may be that we can never reach a firm conclusion in the Committee between option 1 and option 2 and may have to come in with a split report which would have the virtue of allowing both approaches and, I would hope, guaranteeing that the population studies get done.